In the Claims

Applicant has submitted a new complete claim set showing marked up claims with insertions indicated by underlining and deletions indicated by strikeouts.

Please cancel claims 11-19, 21-24, 28 and 30-47 without prejudice or disclaimer.

Please amend pending claims 1-10, 20, 25-27 and 29 as noted below.

1. (Currently Amended) A method for identifying at least one human gene, including mutated or polymorphic variants thereof, which is associated with a mood disorder or related disorder, comprising:

identifying positions of coding regions/genes in ~~Use of~~ an 8.9 cM region of human chromosome 18q disposed between polymorphic markers D18S68 and D18S979 or a fragment thereof that can be compared to the equivalent regions of DNA from a person afflicted with a mood disorder or a related disorder, and ~~for identifying at least one human gene, including mutated or polymorphic variants thereof, which is associated with a mood disorder or related disorder~~.

detecting differences between the coding regions/genes of the 8.9 cM region of human chromosome 18q disposed between polymorphic markers D18S68 and D18S979 or a fragment thereof and equivalent regions in the DNA of an individual afflicted with a mood disorder or related disorder, wherein a difference in the coding regions/genes is an indication that the coding region/gene or mutated or polymorphic variant thereof is associated with the mood disorder or related disorder.

2. (Currently Amended) A method for identifying at least one human gene, including mutated or polymorphic variants thereof, which is associated with a mood disorder or related disorder, comprising:

identifying positions of coding regions/genes in ~~Use of~~ a YAC clone comprising a portion of human chromosome 18q disposed between polymorphic markers D18S60 and D18S61 that can be compared to the equivalent regions of DNA from a person afflicted with a mood disorder or a related disorder, and ~~for identifying at least one human gene, including~~

~~mutated or polymorphic variants thereof, which is associated with a mood disorder or related disorder~~.

detecting differences between the coding regions/genes of the YAC clone comprising a portion of human chromosome 18q disposed between polymorphic markers D18S60 and D18S61 and equivalent regions in the DNA of an individual afflicted with a mood disorder or related disorder, wherein a difference in the coding regions/genes is an indication that the coding region/gene or mutated or polymorphic variant thereof is associated with the mood disorder or related disorder.

3. (Currently Amended) The method of ~~use as claimed in~~ claim 2 wherein said portion comprises the region of chromosome 18q between polymorphic markers D18S68 and D18S979 or a fragment of said region.

4. (Currently Amended) The method of ~~use as claimed in~~ claim 2 wherein said YAC clone is 961_h_9, 942_c_3, 766_f_12, 731_c_7, 907_e_1, 752-g-8 or 717_d_3.

5. (Currently Amended) The method of ~~use as claimed in~~ claim 4 wherein said YAC clone is 961_h_9, 766_f_12 or 907_e_1.

6. (Currently Amended) The method of ~~use as claimed in~~ claim 1 wherein said mood disorder or related disorder is selected from the group consisting of: ~~Diagnostic and Statistical Manual of Mental Disorders, version 4 (DSM-IV) taxonomy and includes~~ mood disorders ~~(296.XX, 300.4, 311, 301, 13, 295.70),~~ schizophrenia and related disorders ~~(295, 297.1, 298.9, 297.3, 298.9)~~, anxiety disorders ~~(300.XX, 309.81, 308.3)~~, adjustment disorders ~~(309, XX)~~ and personality disorders ~~(codes 301. XX)~~.

7. (Currently Amended) A method of identifying at least one human gene, including mutated or polymorphic variants thereof, which is associated with a mood disorder or related disorder which comprises:

detecting nucleotide triplet repeats in a region of human chromosome 18q disposed between polymorphic markers D18S68 and D18S979, wherein the presence of nucleotide triplet repeats in a region of human chromosome 18q disposed between polymorphic markers D18S68 and D18S979 indicates the presence of a human gene, including mutated or polymorphic variants thereof, which is associated with a mood disorder or related disorder.

8. (Currently Amended) A method of identifying at least one human gene, including mutated or polymorphic variants thereof, which is associated with a mood disorder or related disorder comprising: ~~which comprises fragmentation of a YAC clone as defined in claim 2 and detection of nucleotide triplet repeats~~:

transforming a YAC clone with a linearized YAC fragmentation vector containing triplet repeats,

identifying a transformed YAC clone containing triplet repeats,

determining a sequence flanking the triplet repeats, and

comparing the sequence to an equivalent region of DNA from a person afflicted with a mood disorder or a related disorder, wherein a difference in the sequence flanking the triplet repeats and the DNA from the afflicted person is an indication of a human gene or mutated or polymorphic variant thereof that is associated with the mood disorder or related disorder.

9. (Currently Amended) A method as claimed in claim 7 wherein said ~~repeated~~ triplet repeat is CAG or CTG.

10. (Currently Amended) A method as claimed in claim 9 wherein said ~~repeated~~ triplet repeat is detected by means of a probe comprising at least 5 CTG and/or CAG repeats.

11-19. (Cancelled)

20. (Currently Amended) ~~Use of a probe of at least 14 contiguous nucleotides of the cDNA of claim 19 or the complement thereof in a~~ A method for detection in a patient of a

pathological mutation or genetic variation associated with a mood disorder or related disorder, ~~which method comprises~~ comprising:

hybridizing ~~said~~ a probe of at least 14 contiguous nucleotides of a cDNA obtained by the method of claim 7 with a DNA sample from said patient and a DNA sample from a control individual, wherein the cDNA encodes a human protein which if defective is associated with a mood disorder or related disorder and is the expression product of a human gene, including mutated or polypmorphic variants thereof, that is associated with a mood disorder or related disorder, and

comparing the hybridization of the probe to the said patient sample with the hybridization of the probe in the control sample, wherein a difference in the hybridization of the probe in the patient indicates a pathological mutation or genetic variation associated with a mood disorder or related disorder.

21-24. (Cancelled)

25. (Currently Amended) A method of determining the susceptibility of an individual to a mood disorder or related disorder which method comprises:

a) obtaining a DNA sample from said individual;

b) providing primers suitable for the amplification of a nucleotide sequence comprised in the sequences shown in Figure 15a, (SEQ ID NO:12) said primers flanking the trinucleotide repeats comprised in said sequences;

c) applying said primers to the DNA sample and carrying out an amplification reaction;

d) applying said primers to a DNA sample from a control individual and carrying out the amplification reaction; and

e) comparing the results of the amplification reaction for the individual and for the control individual;

wherein the presence of an amplified product that includes a ~~analysing a sample of DNA from that individual for the presence of a~~ DNA polymorphism associated with a mood disorder or related disorder in a region of chromosome 18q disposed between polymorphic markers

D18S68 and D18S979 in the individual sample is an indication of the presence of a susceptibility to a mood disorder or related disorder of said individual.

26. (Currently Amended) A method as in claim ~~claims~~ 25 wherein said DNA polymorphism is a trinucleotide repeat expansion.

27. (Currently Amended) A method as in claim 26 wherein said trinucleotide repeat expansion is comprised in a sequence of nucleotides that differ from the sequence of nucleotides shown in ~~any one of figures~~ figure15a, (SEQ ID NO:12) ~~16a, 17a or 18a~~ only in said trinucleotide repeat expansion.

28. (Cancelled)

29. (Currently Amended) A method as in claim 25 ~~28~~ wherein said nucleotide sequence to be amplified is comprised in the sequence shown in Figure 15a (SEQ ID NO:12) and said primers have the sequences shown in Figure 15b (SEQ ID NOs:13 and 14).

30-47. (Cancelled)